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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/382,096

 DATE: 01/21/2000
 TIME: 13:54:21

Input Set: I382096.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

```

1 <110> APPLICANT: Outtrup, Helle
2           Nielsen, Bjarne Roenfeldt
3           Hedegaard, Lisbeth
4           Andersen, Jens Toenne
5 <120> TITLE OF INVENTION: Alkaline Bacillus Amylase
6 <130> FILE REFERENCE: 5442.400-US
7 <140> CURRENT APPLICATION NUMBER: US/09/382,096
8 <141> CURRENT FILING DATE: 1999-08-24
9 <150> EARLIER APPLICATION NUMBER: 0228/98
10 <151> EARLIER FILING DATE: 1998-02-18
11 <150> EARLIER APPLICATION NUMBER: 60/146,297
12 <151> EARLIER FILING DATE: 1998-02-27
13 <150> EARLIER APPLICATION NUMBER: 09/249,558
14 <151> EARLIER FILING DATE: 1999-02-12
15 <160> NUMBER OF SEQ ID NOS: 4
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
17 <210> SEQ ID NO 1
18 <211> LENGTH: 1646
19 <212> TYPE: DNA
20 <213> ORGANISM: Bacillus sp.
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)...(1646)
24 <221> NAME/KEY: sig_peptide
25 <222> LOCATION: (1)...(93)
26 <221> NAME/KEY: mat_peptide
27 <222> LOCATION: (94)...(1646)
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29     atg caa aac aca gcg aaa aac tcc atc tgg cag agg gtc cgc cac agc      48
30     Met Gln Asn Thr Ala Lys Asn Ser Ile Trp Gln Arg Val Arg His Ser
31         -30          -25          -20
32     gcc att gcc tta tcc gct ctc agt tta tcc ttt ggc ctg cag gcc agc      96
33     Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser
34         -15          -10          -5          1
35     gag tta cca caa att cca cca cag cag gtg aac aac acc atg tac cag      144
36     Glu Leu Pro Gln Ile Pro Pro Gln Gln Val Asn Asn Thr Met Tyr Gln
37             5          10          15
38     gca ttt tat tgg gat gcc tac cct ggc ctt tgg gcc aat tta ccg gcc      192
39     Ala Phe Tyr Trp Asp Ala Tyr Pro Gly Leu Trp Ala Asn Leu Pro Ala
40             20          25          30
41     atg gcg gcc cct ttg gcc gag cgt ggc att acc tcg atg tgg ttg ccg      240
42     Met Ala Ala Pro Leu Ala Glu Arg Gly Ile Thr Ser Met Trp Leu Pro
43             35          40          45
44     ccc gcc gcc aaa ggc atg aat ggt act ttc agt gtc ggt tac gat gta      288

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| | | | | |
|----|---|------|-----|-----|
| 45 | Pro Ala Ala Lys Gly Met Asn Gly Thr Phe Ser Val Gly Tyr Asp Val | | | |
| 46 | 50 | 55 | 60 | 65 |
| 47 | tac gat ttc tgg gat ctg ggc gag ttt aac caa aaa ggc acc acc gcc | 336 | | |
| 48 | Tyr Asp Phe Trp Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Thr Ala | | | |
| 49 | 70 | 75 | 80 | |
| 50 | acc cgt tac ggt act cgt cag cag ctg caa caa gca ctg agt gct ctg | 384 | | |
| 51 | Thr Arg Tyr Gly Thr Arg Gln Gln Leu Gln Gln Ala Leu Ser Ala Leu | | | |
| 52 | 85 | 90 | 95 | |
| 53 | gac caa ctg ggt att cag gcc tat ttt gat gtg gtg ttt aac cac cgc | 432 | | |
| 54 | Asp Gln Leu Gly Ile Gln Ala Tyr Phe Asp Val Val Phe Asn His Arg | | | |
| 55 | 100 | 105 | 110 | |
| 56 | atg ggc gcc gat gca cag gag aat att cct ggc ttt ggc ctg gcc tgg | 480 | | |
| 57 | Met Gly Ala Asp Ala Gln Glu Asn Ile Pro Gly Phe Gly Leu Ala Trp | | | |
| 58 | 115 | 120 | 125 | |
| 59 | acc gag tat cat ctg caa ggt cgt cag gcg cat tat acc cag caa aac | 528 | | |
| 60 | Thr Glu Tyr His Leu Gln Gly Arg Gln Ala His Tyr Thr Gln Gln Asn | | | |
| 61 | 130 | 135 | 140 | 145 |
| 62 | tgg ggc tac ttg tgg cac gac ttt gac tgg aac tgg acc gcg ttt aat | 576 | | |
| 63 | Trp Gly Tyr Leu Trp His Asp Phe Asp Trp Asn Trp Thr Ala Phe Asn | | | |
| 64 | 150 | 155 | 160 | |
| 65 | ggc tcc gac aat cag ctc tac ccc ggc aaa tgg tgg ggc aat acc ttc | 624 | | |
| 66 | Gly Ser Asp Asn Gln Leu Tyr Pro Gly Lys Trp Trp Gly Asn Thr Phe | | | |
| 67 | 165 | 170 | 175 | |
| 68 | cac ttc cct tat ttg atg ggt gag gat gtc gat tac aac cgc ttt gaa | 672 | | |
| 69 | His Phe Pro Tyr Leu Met Gly Glu Asp Val Asp Tyr Asn Arg Phe Glu | | | |
| 70 | 180 | 185 | 190 | |
| 71 | gtg cag cag gaa atg aaa gcc tgg ggc gag tgg atc atc aac agc gtt | 720 | | |
| 72 | Val Gln Gln Glu Met Lys Ala Trp Gly Glu Trp Ile Ile Asn Ser Val | | | |
| 73 | 195 | 200 | 205 | |
| 74 | ggc ttt agc ggc ttt cgg atg gat gcc atc gcc cat gtc gat acc gat | 768 | | |
| 75 | Gly Phe Ser Gly Phe Arg Met Asp Ala Ile Ala His Val Asp Thr Asp | | | |
| 76 | 210 | 215 | 220 | 225 |
| 77 | ttt acc cgt gac tgg atc aat cac gtc cag tgg gcc acc agt gag gat | 816 | | |
| 78 | Phe Thr Arg Asp Trp Ile Asn His Val Gln Trp Ala Thr Ser Glu Asp | | | |
| 79 | 230 | 235 | 240 | |
| 80 | gtg ttc ttt gtc gct gaa gcc tgg gtc agt gat atc aac ggc tat ctg | 864 | | |
| 81 | Val Phe Phe Val Ala Glu Ala Trp Val Ser Asp Ile Asn Gly Tyr Leu | | | |
| 82 | 245 | 250 | 255 | |
| 83 | gat gca gtc aat acg ccg cat ttg cgc gct ttt gat ttc aat ttg cgc | 912 | | |
| 84 | Asp Ala Val Asn Thr Pro His Leu Arg Ala Phe Asp Phe Asn Leu Arg | | | |
| 85 | 260 | 265 | 270 | |
| 86 | gaa gac ttc gtt gct tta agc agc ggt agc aaa gac atg cgt tgg tgg | 960 | | |
| 87 | Glu Asp Phe Val Ala Leu Ser Ser Gly Ser Lys Asp Met Arg Trp Trp | | | |
| 88 | 275 | 280 | 285 | |
| 89 | ggc ggt ctg gtc aat agc cag cac cgt gat cgg gcg gtc act ttt gtc | 1008 | | |
| 90 | Gly Gly Leu Val Asn Ser Gln His Arg Asp Arg Ala Val Thr Phe Val | | | |
| 91 | 290 | 295 | 300 | 305 |
| 92 | gat aac cac gat acc agc cgg gcc ggc aac cct tat ggc atg ccg cag | 1056 | | |
| 93 | Asp Asn His Asp Thr Ser Arg Ala Gly Asn Pro Tyr Gly Met Pro Gln | | | |
| 94 | 310 | 315 | 320 | |

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| | | |
|-----|---|------|
| 95 | gtg atc aac tac aag aac cag gcc tac gct tac att ctg ttg cgt gag | 1104 |
| 96 | Val Ile Asn Tyr Lys Asn Gln Ala Tyr Ala Tyr Ile Leu Leu Arg Glu | |
| 97 | 325 330 335 | |
| 98 | cat ggg gtg ccg act gtg ttt gcc cgc gat tac gac gaa ttt ggc atg | 1152 |
| 99 | His Gly Val Pro Thr Val Phe Ala Arg Asp Tyr Asp Glu Phe Gly Met | |
| 100 | 340 345 350 | |
| 101 | gcf cca acg ctg gat aaa ttg att gag gcf cgc cgc tac ttt gct tat | 1200 |
| 102 | Ala Pro Thr Leu Asp Lys Leu Ile Glu Ala Arg Arg Tyr Phe Ala Tyr | |
| 103 | 355 360 365 | |
| 104 | ggt cct ggc cat gag tac tcc ggc aat acc gag gcc gtc tac gcc tat | 1248 |
| 105 | Gly Pro Gly His Glu Tyr Ser Gly Asn Thr Glu Ala Val Tyr Ala Tyr | |
| 106 | 370 375 380 385 | |
| 107 | gtg cgc gaa ggg ctt agc act gtg ccg ggt acc ggt ctg gtg atg ctg | 1296 |
| 108 | Val Arg Glu Gly Leu Ser Thr Val Pro Gly Thr Gly Leu Val Met Leu | |
| 109 | 390 395 400 | |
| 110 | ata tcg ggt cga aac tgg ggt cag cag tcg ttc acc atc aac agc | 1344 |
| 111 | Ile Ser Gly Arg Asn Trp Gly Gly Gln Gln Ser Phe Thr Ile Asn Ser | |
| 112 | 405 410 415 | |
| 113 | cac cag ccg aat acc acc ttt tac gat tat acc ggc aat gtt agc ggc | 1392 |
| 114 | His Gln Pro Asn Thr Thr Phe Tyr Asp Tyr Thr Gly Asn Val Ser Gly | |
| 115 | 420 425 430 | |
| 116 | acg gtg acc acc aat gcg cag ggc tat ggc agc ttc ccg gtc act atg | 1440 |
| 117 | Thr Val Thr Thr Asn Ala Gln Gly Tyr Ser Phe Pro Val Thr Met | |
| 118 | 435 440 445 | |
| 119 | acg gaa agt acc ggt tgg tca gtc tgg gta cca caa tcc aat ggt ggc | 1488 |
| 120 | Thr Glu Ser Thr Gly Trp Ser Val Trp Val Pro Gln Ser Asn Gly Gly | |
| 121 | 450 455 460 465 | |
| 122 | act cag ccg gga tcc att acc ctg cgg atg acc aag gat gtt ggc tat | 1536 |
| 123 | Thr Gln Pro Gly Ser Ile Thr Leu Arg Met Thr Lys Asp Val Gly Tyr | |
| 124 | 470 475 480 | |
| 125 | ggc ttt tcg ttg ttc acc ggc agc agt gcg gaa ctg acc aac tgg | 1584 |
| 126 | Gly Phe Ser Leu Phe Phe Thr Gly Ser Ser Ala Glu Leu Thr Asn Trp | |
| 127 | 485 490 495 | |
| 128 | ggc ggc ggt att gaa ggc acc tgg aca tcc ggt aat gtc tgg gaa gtg | 1632 |
| 129 | Gly Gly Gly Ile Glu Gly Thr Trp Thr Ser Gly Asn Val Trp Glu Val | |
| 130 | 500 505 510 | |
| 131 | acc atc ccg gat cc | 1646 |
| 132 | Thr Ile Pro Asp | |
| 133 | 515 | |
| 134 | <210> SEQ ID NO 2 | |
| 135 | <211> LENGTH: 548 | |
| 136 | <212> TYPE: PRT | |
| 137 | <213> ORGANISM: Bacillus sp. | |
| 138 | <220> FEATURE: | |
| 139 | <221> NAME/KEY: SIGNAL | |
| 140 | <222> LOCATION: (1)...(31) | |
| 141 | <400> SEQUENCE: 2 | |
| 142 | Met Gln Asn Thr Ala Lys Asn Ser Ile Trp Gln Arg Val Arg His Ser | |
| 143 | -30 -25 -20 | |
| 144 | Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser | |

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 | -15 | -10 | -5 | 1 | | | | | | | | | | | | |
| 146 | Glu | Leu | Pro | Gln | Ile | Pro | Pro | Gln | Gln | Val | Asn | Asn | Thr | Met | Tyr | Gln |
| 147 | | | | | | | 5 | | | 10 | | | | | 15 | |
| 148 | Ala | Phe | Tyr | Trp | Asp | Ala | Tyr | Pro | Gly | Leu | Trp | Ala | Asn | Leu | Pro | Ala |
| 149 | | | | | | | 20 | | | 25 | | | | | 30 | |
| 150 | Met | Ala | Ala | Pro | Leu | Ala | Glu | Arg | Gly | Ile | Thr | Ser | Met | Trp | Leu | Pro |
| 151 | | | | | | | 35 | | | 40 | | | | 45 | | |
| 152 | Pro | Ala | Ala | Lys | Gly | Met | Asn | Gly | Thr | Phe | Ser | Val | Gly | Tyr | Asp | Val |
| 153 | | | | | | 50 | | | 55 | | | 60 | | | 65 | |
| 154 | Tyr | Asp | Phe | Trp | Asp | Leu | Gly | Glu | Phe | Asn | Gln | Lys | Gly | Thr | Thr | Ala |
| 155 | | | | | | 70 | | | 75 | | | | | 80 | | |
| 156 | Thr | Arg | Tyr | Gly | Thr | Arg | Gln | Gln | Leu | Gln | Gln | Ala | Leu | Ser | Ala | Leu |
| 157 | | | | | | 85 | | | 90 | | | | | 95 | | |
| 158 | Asp | Gln | Leu | Gly | Ile | Gln | Ala | Tyr | Phe | Asp | Val | Val | Phe | Asn | His | Arg |
| 159 | | | | | | 100 | | | 105 | | | | | 110 | | |
| 160 | Met | Gly | Ala | Asp | Ala | Gln | Glu | Asn | Ile | Pro | Gly | Phe | Gly | Leu | Ala | Trp |
| 161 | | | | | | 115 | | | 120 | | | | | 125 | | |
| 162 | Thr | Glu | Tyr | His | Leu | Gln | Gly | Arg | Gln | Ala | His | Tyr | Thr | Gln | Gln | Asn |
| 163 | | | | | | 130 | | | 135 | | | 140 | | | 145 | |
| 164 | Trp | Gly | Tyr | Leu | Trp | His | Asp | Phe | Asp | Trp | Asn | Trp | Thr | Ala | Phe | Asn |
| 165 | | | | | | 150 | | | 155 | | | | | 160 | | |
| 166 | Gly | Ser | Asp | Asn | Gln | Leu | Tyr | Pro | Gly | Lys | Trp | Trp | Gly | Asn | Thr | Phe |
| 167 | | | | | | 165 | | | 170 | | | | | 175 | | |
| 168 | His | Phe | Pro | Tyr | Leu | Met | Gly | Glu | Asp | Val | Asp | Tyr | Asn | Arg | Phe | Glu |
| 169 | | | | | | 180 | | | 185 | | | | | 190 | | |
| 170 | Val | Gln | Gln | Glu | Met | Lys | Ala | Trp | Gly | Glu | Trp | Ile | Ile | Asn | Ser | Val |
| 171 | | | | | | 195 | | | 200 | | | | | 205 | | |
| 172 | Gly | Phe | Ser | Gly | Phe | Arg | Met | Asp | Ala | Ile | Ala | His | Val | Asp | Thr | Asp |
| 173 | | | | | | 210 | | | 215 | | | 220 | | | 225 | |
| 174 | Phe | Thr | Arg | Asp | Trp | Ile | Asn | His | Val | Gln | Trp | Ala | Thr | Ser | Glu | Asp |
| 175 | | | | | | 230 | | | 235 | | | | | 240 | | |
| 176 | Val | Phe | Phe | Val | Ala | Glu | Ala | Trp | Val | Ser | Asp | Ile | Asn | Gly | Tyr | Leu |
| 177 | | | | | | 245 | | | 250 | | | | | 255 | | |
| 178 | Asp | Ala | Val | Asn | Thr | Pro | His | Leu | Arg | Ala | Phe | Asp | Phe | Asn | Leu | Arg |
| 179 | | | | | | 260 | | | 265 | | | | | 270 | | |
| 180 | Glu | Asp | Phe | Val | Ala | Leu | Ser | Ser | Gly | Ser | Lys | Asp | Met | Arg | Trp | Trp |
| 181 | | | | | | 275 | | | 280 | | | | | 285 | | |
| 182 | Gly | Gly | Leu | Val | Asn | Ser | Gln | His | Arg | Asp | Arg | Ala | Val | Thr | Phe | Val |
| 183 | | | | | | 290 | | | 295 | | | 300 | | | 305 | |
| 184 | Asp | Asn | His | Asp | Thr | Ser | Arg | Ala | Gly | Asn | Pro | Tyr | Gly | Met | Pro | Gln |
| 185 | | | | | | 310 | | | 315 | | | | | 320 | | |
| 186 | Val | Ile | Asn | Tyr | Lys | Asn | Gln | Ala | Tyr | Ala | Tyr | Ile | Leu | Leu | Arg | Glu |
| 187 | | | | | | 325 | | | 330 | | | | | 335 | | |
| 188 | His | Gly | Val | Pro | Thr | Val | Phe | Ala | Arg | Asp | Tyr | Asp | Glu | Phe | Gly | Met |
| 189 | | | | | | 340 | | | 345 | | | | | 350 | | |
| 190 | Ala | Pro | Thr | Leu | Asp | Lys | Leu | Ile | Glu | Ala | Arg | Arg | Tyr | Phe | Ala | Tyr |
| 191 | | | | | | 355 | | | 360 | | | | | 365 | | |
| 192 | Gly | Pro | Gly | His | Glu | Tyr | Ser | Gly | Asn | Thr | Glu | Ala | Val | Tyr | Ala | Tyr |
| 193 | | | | | | 370 | | | 375 | | | 380 | | | 385 | |
| 194 | Val | Arg | Glu | Gly | Leu | Ser | Thr | Val | Pro | Gly | Thr | Gly | Leu | Val | Met | Leu |

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| | | | | |
|-----|---|-----|-----|-----|
| 195 | 390 | 395 | 400 | |
| 196 | Ile Ser Gly Arg Asn Trp Gly Gly Gln Gln Ser Phe Thr Ile Asn Ser | | | |
| 197 | 405 | 410 | 415 | |
| 198 | His Gln Pro Asn Thr Thr Phe Tyr Asp Tyr Thr Gly Asn Val Ser Gly | | | |
| 199 | 420 | 425 | 430 | |
| 200 | Thr Val Thr Thr Asn Ala Gln Gly Tyr Gly Ser Phe Pro Val Thr Met | | | |
| 201 | 435 | 440 | 445 | |
| 202 | Thr Glu Ser Thr Gly Trp Ser Val Trp Val Pro Gln Ser Asn Gly Gly | | | |
| 203 | 450 | 455 | 460 | 465 |
| 204 | Thr Gln Pro Gly Ser Ile Thr Leu Arg Met Thr Lys Asp Val Gly Tyr | | | |
| 205 | 470 | 475 | 480 | |
| 206 | Gly Phe Ser Leu Phe Phe Thr Gly Ser Ser Ala Glu Leu Thr Asn Trp | | | |
| 207 | 485 | 490 | 495 | |
| 208 | Gly Gly Gly Ile Glu Gly Thr Trp Thr Ser Gly Asn Val Trp Glu Val | | | |
| 209 | 500 | 505 | 510 | |
| 210 | Thr Ile Pro Asp | | | |
| 211 | 515 | | | |
| 212 | <210> SEQ ID NO 3 | | | |
| 213 | <211> LENGTH: 1764 | | | |
| 214 | <212> TYPE: DNA | | | |
| 215 | <213> ORGANISM: Bacillus sp. | | | |
| 216 | <220> FEATURE: | | | |
| 217 | <221> NAME/KEY: CDS | | | |
| 218 | <222> LOCATION: (1)...(1764) | | | |
| 219 | <221> NAME/KEY: sig_peptide | | | |
| 220 | <222> LOCATION: (1)...(93) | | | |
| 221 | <221> NAME/KEY: mat_peptide | | | |
| 222 | <222> LOCATION: (94)...(1764) | | | |
| 223 | <400> SEQUENCE: 3 | | | |
| 224 | atg caa aac aca gcg aaa aac tcc atc tgg cag agg gtg cgc cac agc | | 48 | |
| 225 | Met Gln Asn Thr Ala Lys Asn Ser Ile Trp Gln Arg Val Arg His Ser | | | |
| 226 | -30 | -25 | -20 | |
| 227 | gcc att gcc tta tcc gct ctc agt tta tcc ttt ggc ctg cag gcc agc | | 96 | |
| 228 | Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser | | | |
| 229 | -15 | -10 | -5 | 1 |
| 230 | gag tta cca caa att cca cca cag cag gtg aac aac acc atg tac cag | | 144 | |
| 231 | Glu Leu Pro Gln Ile Pro Pro Gln Gln Val Asn Asn Thr Met Tyr Gln | | | |
| 232 | 5 | 10 | 15 | |
| 233 | gca ttt tat tgg gat gcc tac cct ggc ctt tgg gcc aat tta ccg gcc | | 192 | |
| 234 | Ala Phe Tyr Trp Asp Ala Tyr Pro Gly Leu Trp Ala Asn Leu Pro Ala | | | |
| 235 | 20 | 25 | 30 | |
| 236 | atg gcg gcc cct ttg gcc gag cgt ggc att acc tcg atg tgg ttg ccg | | 240 | |
| 237 | Met Ala Ala Pro Leu Ala Glu Arg Gly Ile Thr Ser Met Trp Leu Pro | | | |
| 238 | 35 | 40 | 45 | |
| 239 | ccc gcc gcc aaa ggc atg aat ggt act ttc agt gtc ggt tac gat gta | | 288 | |
| 240 | Pro Ala Ala Lys Gly Met Asn Gly Thr Phe Ser Val Gly Tyr Asp Val | | | |
| 241 | 50 | 55 | 60 | 65 |
| 242 | tac gat ttc tgg gat ctg ggc gag ttt aac caa aaa ggc acc acc gcc | | 336 | |
| 243 | Tyr Asp Phe Trp Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Thr Ala | | | |
| 244 | 70 | 75 | 80 | |

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VERIFICATION SUMMARY
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DATE: 01/21/2000
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Line ? Error/Warning

Original Text

333 W Line data has been corrected

Thr Asn Leu His Pro Ser Phe Asn Gly Gly P